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FIG. 1 - AOPRT-L CDNA sequence

	ATGGCTCTATCCAAAGCTTTCACCTCCTCCTCCTCCTCCTCCTCCCTC	150	ACCGTCACCAACAAATGCACCTACACCGGGGCGCGGGGGGGG	230	TCCTGGACCCTCACCGTCGCCCCGGTGCCCGCATCTGGGGCCGAACCGGCTGCTCCTTCGACCCCTCT S W T L T V A P G T T G A R I W G R T G C S F D P S	240 250 260 270 280 290 300 310 310 310 310 310 310 310 310 31
70 -	A T	H — 6			CGACC D F	CGAC!
);ccc) 8	CGAC	220	CTTC	300 - P
	SCCTC	140 	rgcc1	~ -	rgcr S S	rccc(
9 -	L A		CGCC R F		ე ე ე	290
	70000	130	විටදිල්	210	3AAC	25
50	CACCTCCTCTTCTTCTTCTTCTTGCCCTCGCCTCGCCGCCAC	- i —	CACACCGGALLCUGUS CTACACCGTCTGGGCGCTGCGGGGGGGGGGGGCGCCTCGACCCCAACC		CCCCGGTACCACCGGTGCCGATCTGGGGCCGAACCGGCTGCTCCTTCGACCC	260 270 280 300 300
	OCTO DIA		0000 60000	200	CTGG W	280 - CTGC2
40	crer	120	CAGT	7 —	GCAT	orrigo
4 -	L P	ţ	SGCTG A A		FGCC A F	270 GTCTCC
	rccrc L	110	000 000 000 000	190	ეეე ე	, 9 9 9 9
30	CTCC	, , , , , , , , , , , , , , , , , , ,	GTCT(V W		ACCA T T	0 11 13 13 13 13 13 13 13 13 13 13 13 13
	CTCC S	0	7.0400	180	CGGT	260 - D C
50	rtcac	100	ACCTA	P 2	3000 A	ACCG(
	AGCTT		41602 0 0	170 	CGTCC V	250
0	GGCTCTATCCAAAGCTT' A L S K A F	06	ACAA K	1 	TCAC	ATTG
10	CTAT(L S	•	ACCA.	a 0	ACCC T L	240 CGGCC GH
	GGCT	. — 80 — 80	ACCGTCACCAAATGCACCTACACCGGAACCCGGGGGGGGG	160 170 170 170	TCCTGGACCCTCACCGTCG S W T L T V A	240 250 sccacgccattgccaga H G H C Q T
	AT M	& —	AC T	័ ភ្ជ	S S	ဗ ဗ

390	ATG M		cro		ე ე	0	ACT T	700 	
380	GCAGAATTCGCCCTGAACCAGTACGCCGGCCAGGACTTCTACGACTCCCTCGTCGACGGCTTCAACATCCCCATG A E F A L N Q Y A G Q D F Y D I S L V D G F N I P M	460	CGCGGAG A E	540	AAGCACCCGGGGGGGGTGTAACACCGTGTTCAAGACCAATGAGTACTGCTGCACTTCGGGAGGCTGTGGG	620	CCCACGGACTATTCCAAGTTTTCAAGCAGAGGTGCCTGATGACGCTAACGGATGACGCTACCAGCACT P T D Y S K F F K Q R C P D A Y S Y P K D D A T S T	630 640 650 700 680 690 700 	770 - CC
	G F N	450	CAGTGCCC	530	ACTTCGGG T S G	610	SGATGACG D D A	690 :AGATGTTG) CTACTTGA
370	TCGTCGAC V D		TATCAACGGI I N G	520 	ACTGCTGC C C	600	TACCCCAAC Y P K	680 	760 GTAAGCTC
360	CATCTCCCT I S L	440	CGCGGACA A D I	·	CAATGAGT N E Y	290	GCGTACAGTT A Y S Y	670 TTGATCGA	730 740 750 760 77
350	TTCTACGA(F Y D	430	CGGTGCAC	510	TTCAAGAC F K T	S —	CCTGATGC P D A	660 	740 cggaataa
40	CCAGGAC	420	ACGACATCO D I	200	SCACCGTG T V	580	AGAGGTGC R C	6 	730 Cattaagaa
- m	TACGCCGC Y A G	10	AATTGCCP N C H	490	AACCCGTC N P C	570	TTCAAGC	650 	7. CTAGCTC
330	TGAACCAG N Q	41	CGTCCGGA S G	0	GGTGTAAC C N	560	CCAAGTT	640 - G A	720 ATTTGTAC
320	ATTCGCCCTGAA F A L N	400	CTTCTCCCGACGTC F S P T S	480	5 5 d		CACGGACTATTCCA T D Y S K	630 64 TACTTGTCCCAGTGC T C P S G	710 CAAACTATGGTTAATTTGTA
	GCAGAA A E		GACTIC D F	470	AAGGC? K A	550	CCCACC P T	f TTTACT	CAAAC1

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Similarity of AoPRT-L to other PR-5 Group Proteins

Protein	Cellular Location	Id	Percentage Similarity or Identity to AoPRT-L	ntage r <u>Identity</u> pPRT-L
AoPRT-L	Extracellular	4.9	100	100
Osmotin	Vacuolar	7.5	86	. 77
Pobacco Osmotin-like	Vacuolar	7.5	68	77
Pobacco Thaumatin-like	Extracellular	5.2	80	80
Fomato NP24	Vacuolar	7.8	78	65
Fhaumatin	Cytoplasmic	12.0	9/	63
Potato Osmotin-like	6.	6.1	9/	62
Rice Thaumatin-like	ز	5.0	70	53
Wheat Thaumatin-like	Extracellular	4.5	89	49
Barley Thaumatin-like	Extracellular	4.2	<i>L</i> 9	49

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FIG.3a

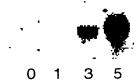
Induction of AoPRT-L following cell isolation



Time after isolation (days)

FIG.3b

Induction in etiolated seedlings by wounding

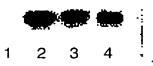


Time after wounding (davs)
Explant length 5mm

FIG.3c

Induction of AoPRT-L in whole plants by SA

Time course of induction following foliar application of 1mM SA to whole plants



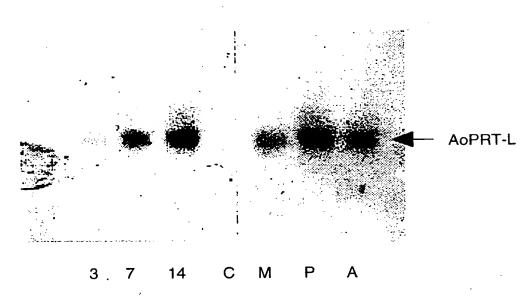


- 1; Water treated
- 2; 3 days after foliar spraying with 1mM SA
- 3; 3 days after continuous root feeding with 1mM SA
- 4; 3 days after initial root feeding with 1mM SA

Time after application (days)

FIG.4

AoPRT-L Expression in Asparagus seedlings infected with *Stemphyllium versicarium*



Figures (3, 7 & 14) indicate days after symptom development

- C uninfected Asparagus
- M Infected region (day 14)
- P Pigmented region (day 14)
- A Asymptomatic region (day 14)

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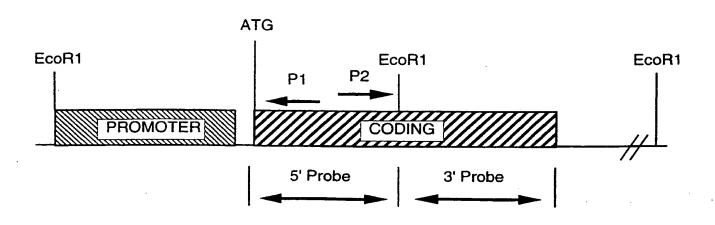
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FIG. 5 IPCR Strategy

Southern Analysis

•	Asp [DNA x EcoF	₹1
	Full cDNA	5' Probe	3' Probe
2.5 kb	-		
0.8 kb			÷

Primer Design



	AoPRT-L Promoter sequence: Similarities with other Defence Genes	milarities with o	other Defence Ge	nes
-472	GAATTCTTAT TGCGACCTGA CTCTCTTGTT		GTGCTGCCGA GGTGCTGTCG	GGTGCTGTCG
-422	AAATTTCTGT TGCGCACAAC	ATACTGGTCC	TTGCTTGATT	TGACAGTTCC
-372	AATAATTATT TCCATGTCAT GAGAGAAGCA CATGACTAAA GTAATTAGCT	SAGAGAAGCA	CATGACTAAA	GTAATTAGCT
-322	TAATCCCCTA AAACTCAATA	CAAACGAGAT	GACACATCCA CAGAAAAAT	CAGAAAAAAT
-272	TCTAATTAGT CTTTGCGTGT	AGAAATTGGA	AGAAATTGGA AACTGAATAC CTACATTAAT	CTACATTAAT
-222	TACAACTTT GCAAATAAAA	TATAAAGAAA	TATAAAGAAA GTTCTAACAT GAAGACTAGT	GAAGACTAGT
-172	TCTAACATGA AGACTAGTCC	ACGAACTCGT	ACCTTATTCC ACAAAGGCTT	ACAAAGGCTT
-122	AGACTTTCCA CAAATCGAGA TTATCCCATG GACTGATGGA CACCATCCAA	TTATCCCATG	GACTGATGGA	CACCATCCAA
-72	ATTATCCOTA TAAATACCTG CCCATTCCCC TCCTCCAGAC TCATCTAACT	CCCATTCCCC	TCCTCCAGAC	TCATCTAACT
-22	CAAAAACAAC ACACAACCAA TCATG	TCATG		
				FIG. 6
	Potato Wound-Induced		18 bp repeat	
	Tobacco PR-2	T.	TATA Box	
	Carrot PR-3 and PR-4	-4		

pIPCR-TA

PCR using 5' and 3' primers Clone into pJIT60 using KpnI and PstI

p22-JIT60
Clone in GUS(INT) using BamHI and EcoRI

p22-GUS(INT) JIT60

Cut with KpnI and XhoI and clone into KpnI and SalI cut pBin19

p22-GUS(INT) Bin19

FIG. 7

FIG.8

Histochemical localistion of GUS activity in untreated stems from transgenic tobacco harbouring AoPRT-L-GUS or PR-1a-GUS

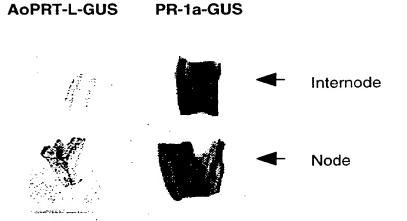
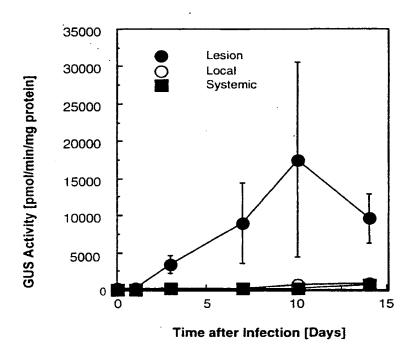
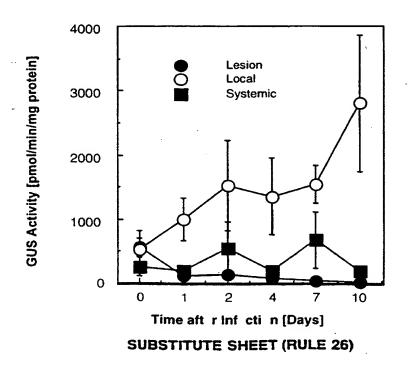


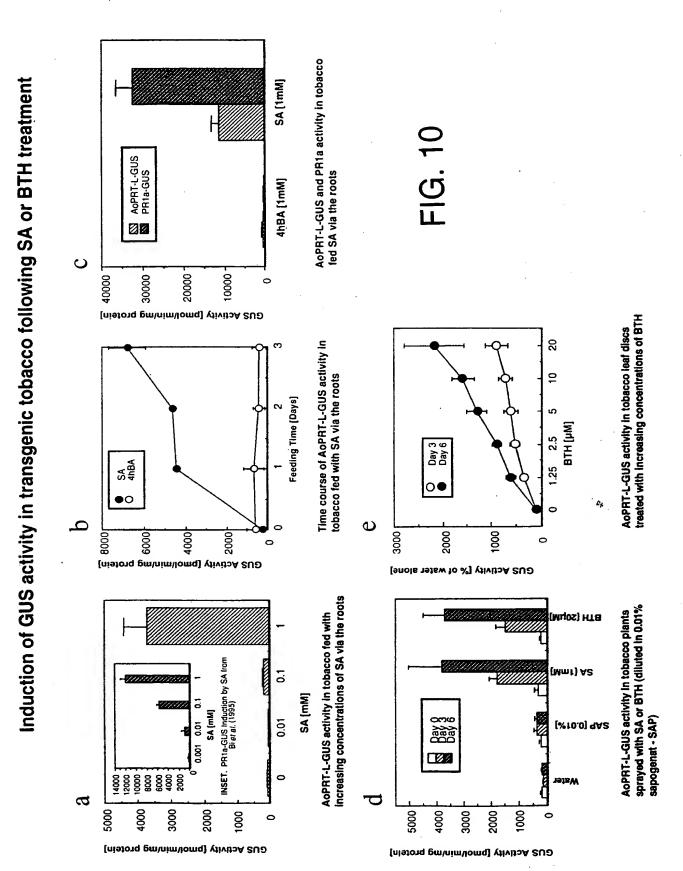
FIG. 9

AoPRT-L-GUS Expression in TMV-infected Tobacco

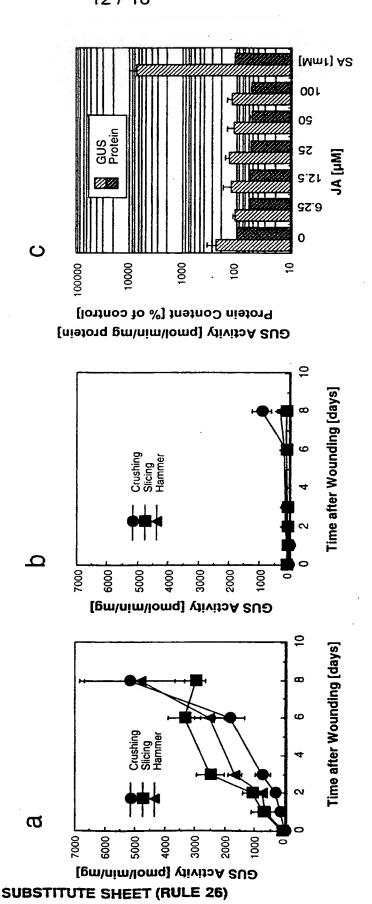


AoPRT-L-GUS Expression in Tobacco infected with *Pseudomonas* syringae pathovar phaseolicola

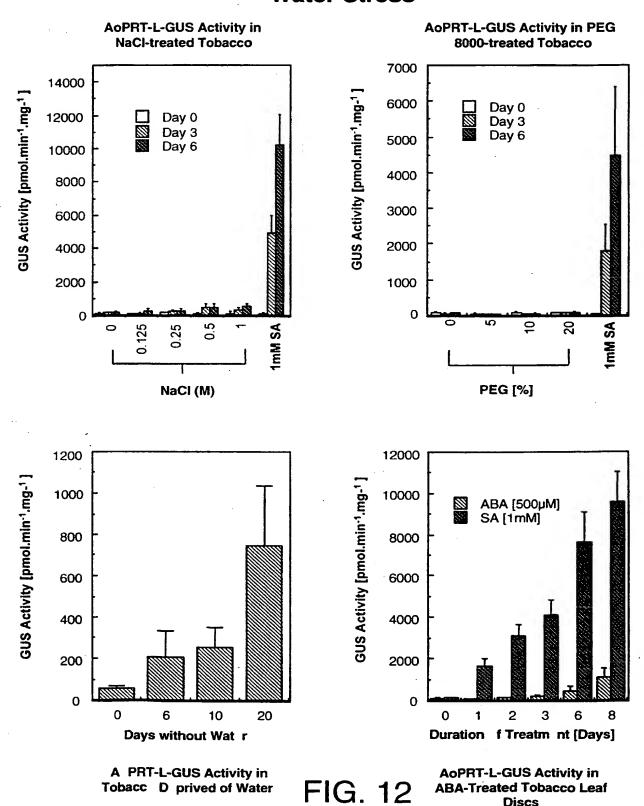




Effects of wounding and JA on GUS expression in FIG. 11 transgenic plants

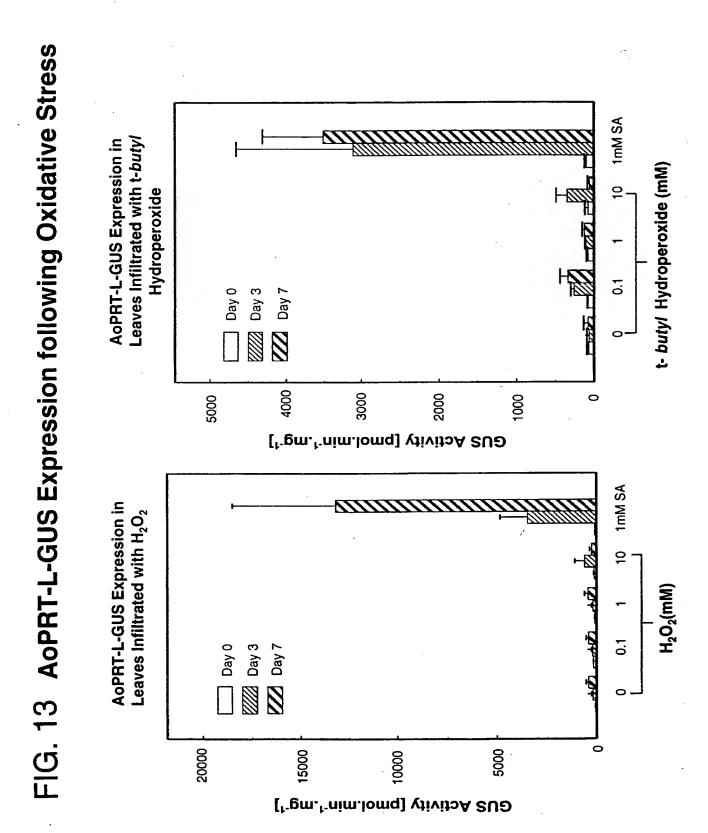


AoPRT-L-GUS Expression Following Water Stress



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Discs



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FIG. 14

AoPRT-L-GUS and Pr1a-Gus expression after SA or BTH induction in Brassica napus leaves

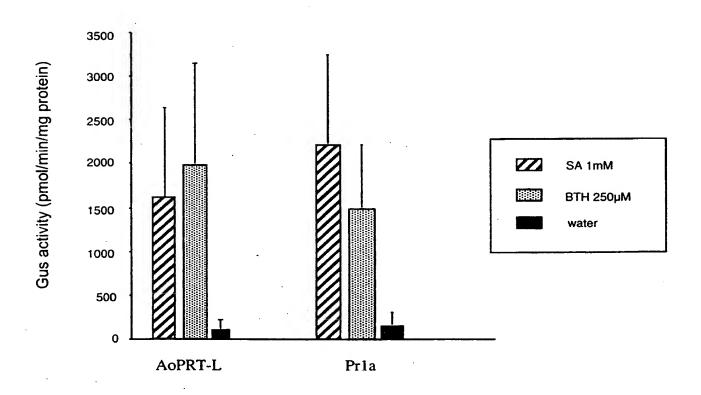


FIG. 15a AoPRT-L promoter deletions

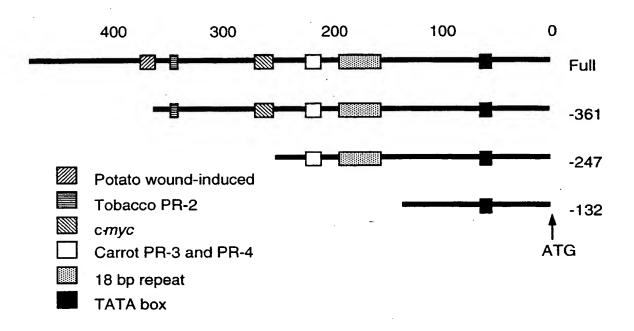
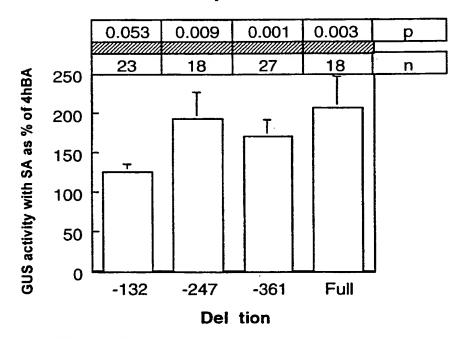


FIG. 15b SA-responsiveness of AoPRT-L promoter deletion-GUS constructs in T0 transgenic tobacco plants



n - number of individual transformants

p - probability that activity with SA is not different to activity with control-treatment (Wilcoxon signed rank test)

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ATG Multimerised AoPRT-Lx3 SA-responsive promoter AoPRT-L-min TATA Box (-132 to -1) The -247 to -133 putative SA-reponsive region cloned into pJIT-60 GUS (INT) containing the AoPRT-L minimal promoter (-132 to -1) FIG. 15c 18bp Repeat AoPRT-L-SA (-247 to -133) Carrot PR-3 & PR-4

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FIG. 16 schematic diagram of plasmid pGB24

